Supplement for: "Large single-locus effects for maturation timing are mediated via condition variation in Atlantic salmon"

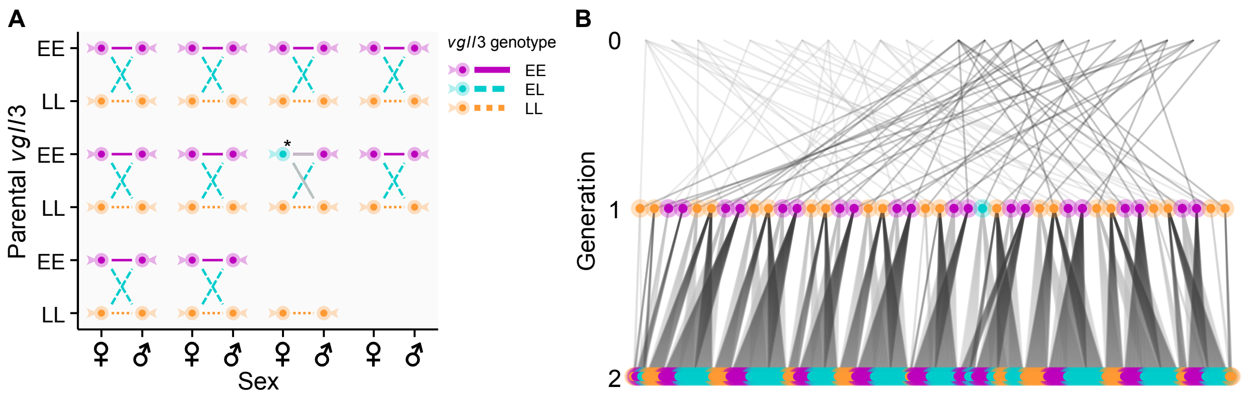

Fig. S1. Realized breeding design and pedigree for the experimental Atlantic salmon population. The realized breeding design in **A** shows that an anticipated 2x2 factorial for *vgll3* homozygous dams by *vgll3* homozygous sires was successful for nine factorials, but one factorial curtailed because of low egg survival, whereas one dam (marked by asterisk) was determined to be *vgll3* heterozygous upon re-genotyping using fin clips taken at spawning. The pedigree in **B** depicts the relationships for the studied salmon (generation 2; N = 5,145; only every 10th individual plotted to facilitate viewing) via parents (generation 1) up to their grandparents (generation 0). Upward links to dams and sires in the pedigree are colored in light and dark gray, respectively. *Vgll3* genotypes for created families (lines) and breeders (fish shapes) in **A** or generations 1 and 2 in **B** (circles) are depicted corresponding to the legend.

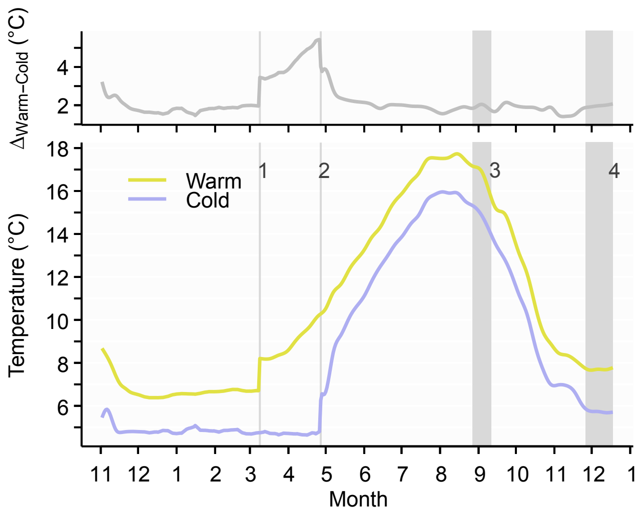

Fig. S2. Experienced water temperatures in the experimental Atlantic salmon cohort and resulting water temperature differences between the warm and cold temperature environments. The upper panel shows the temperature difference between the warm and cold temperature environments, whereas the lower panel shows the underlying temperatures. Experimental events in the lower panel are indicated by light gray vertical lines with **1**: transfer from egg incubators to tanks and first feeding in the warm environment; **2**: transfer from egg incubators to tanks and first feeding in the cold environment; **3**: phenotyping of length and condition as used in analyses described in the manuscript; **4**: maturation status and sex confirmation assessments.

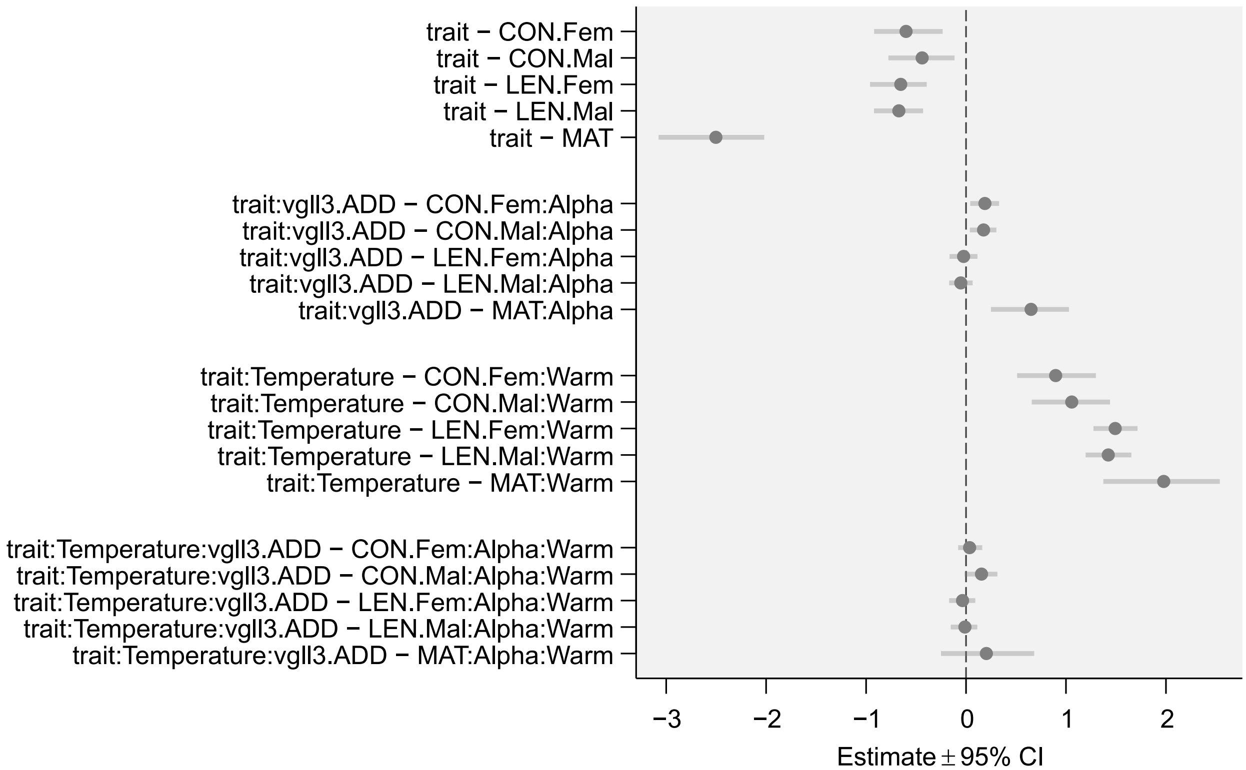

Fig. S3. Temperature-by-*vgll3* effects were not detected for maturation and its component traits. The figure shows mean effect (given as term – term level) estimates with 95% credible intervals for the multivariate animal model on traits of male maturation (MAT), male length (LEN.Mal), female length (LEN.Fem), male condition (CON.Mal), and female condition (CON.Fem) with additive *vgll3*-by-temperature effects. Traits were modelled as a linear function of temperature effects (factor: cold, warm), additive *vgll3* effect (vgll3.ADD; for EE, EL, LL; alpha = 1, 0, -1), and temperature-by-additive *vgll3* effect. Temperature-by-additive *vgll3* effects for all traits were removed for the final model because their 95% credible intervals included zero.

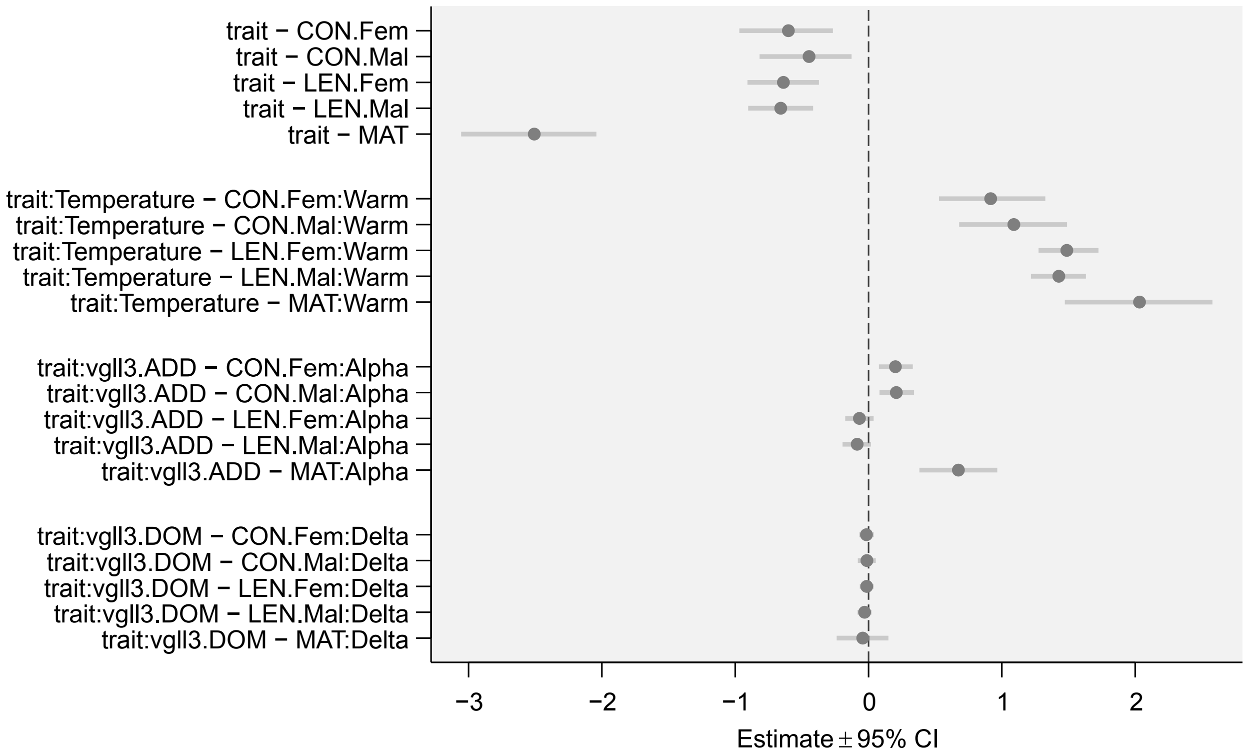

Fig. S4. Dominance effects were not detected for maturation and its component traits. The figure shows mean effect (given as term – term level) estimates with 95% credible intervals for the multivariate animal model on traits of male maturation (MAT), male length (LEN.Mal), female length (LEN.Fem), male condition (CON.Mal), and female condition (CON.Fem) with dominance effects. Traits were modelled as a linear function of temperature effects (factor: cold, warm), additive *vgll3* effect (vgll3.ADD; for EE, EL, LL; alpha = 1, 0, -1), and dominant *vgll3* effect (vgll3.DOM; for EE, EL, LL; alpha = 0, 1, 0). Dominance effects for all traits were removed for the final model because their 95% credible intervals included zero.

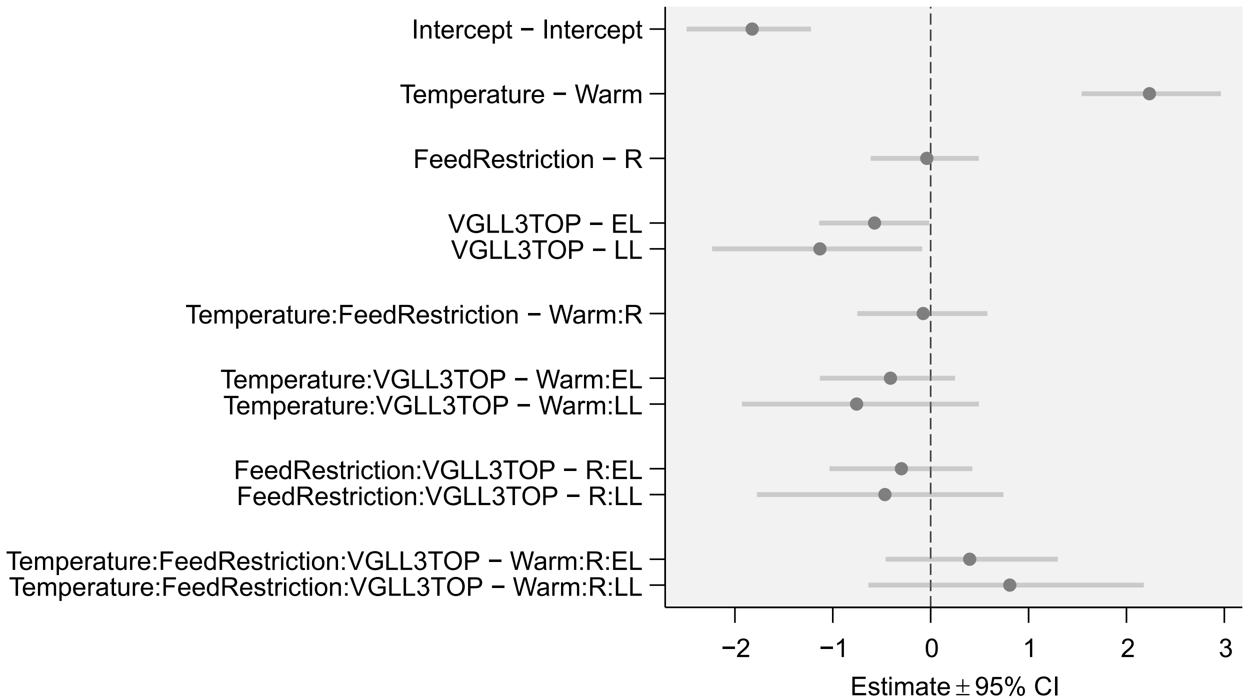

Fig. S5. Feed treatment effects were not detected for maturation probability. The figure shows mean effect (given as term – term level) estimates with 95% credible intervals for the univariate threshold model on male maturation binaries with initial mean effect structure. Maturation binaries were modelled as a linear function of *vgll3* genotype (factor: EE, EL, LL), temperature (factor: cold, warm), feed restriction (factor: R = restricted, F = full feeding), and all interactions. All feed treatment effects were removed for a reduced model because their 95% credible intervals included zero.

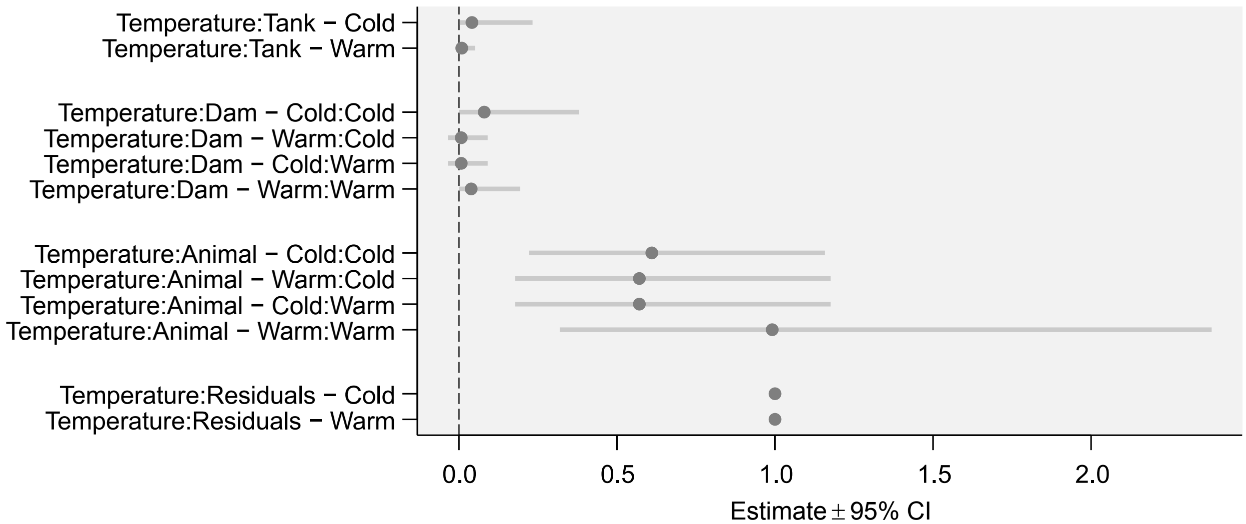

Fig. S6. Dam and tank effects were not detected for maturation probability. The figure shows covariance effect (given as term – term level) estimates for the univariate threshold model on male maturation binaries with the reduced final mean effect structure. Maturation binaries were modelled as a linear function of *vgll3* genotype (factor: EE, EL, LL) and temperature (factor: cold, warm). This model included covariances for dam effects that were removed for the final model because their 95% credible intervals included zero. Variance terms for tank effects were retained, although their estimate 95% credible intervals included zero, because tank effects reflect the experimental design. Residual variance in each environment was fixed at one to make additive genetic (animal) effect variance estimable. As a result, all (co)variance estimates are scaled relative to a residual variance of one and absolute estimates cannot be compared between environments.

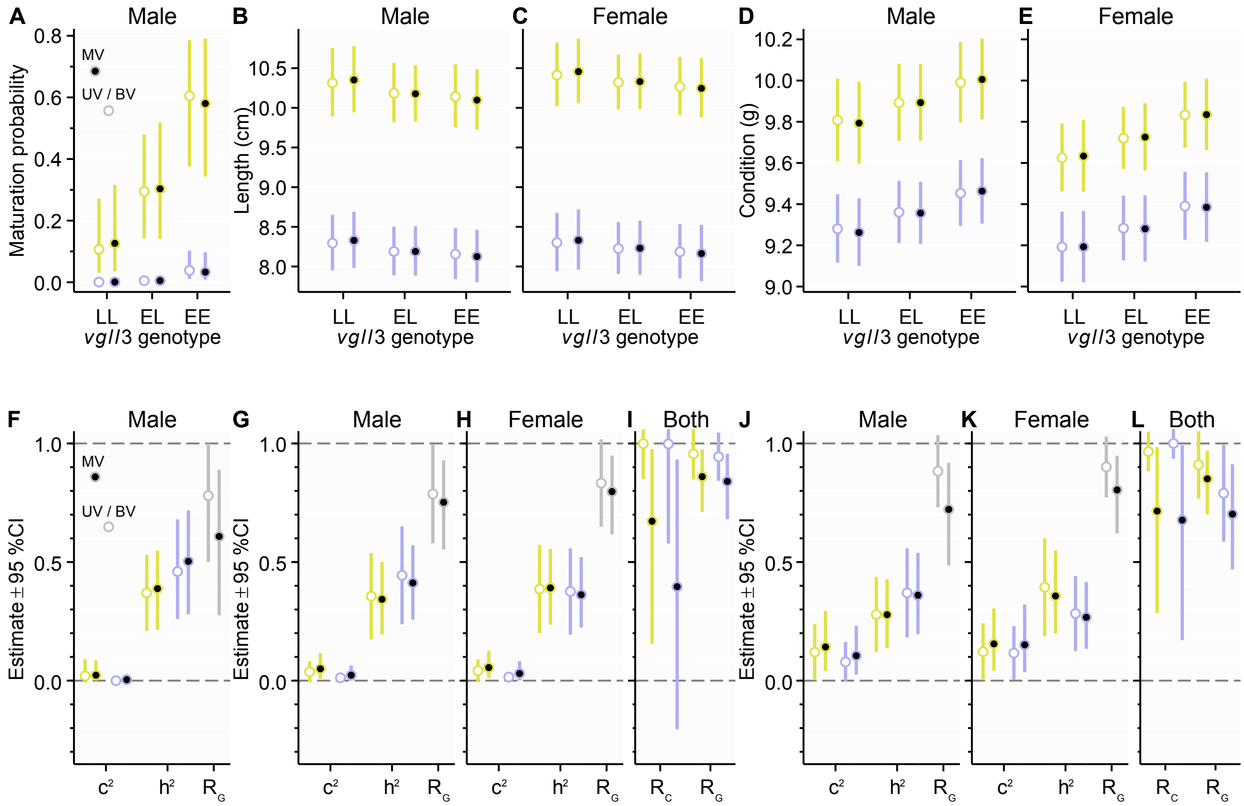

Fig. S7. Comparison between univariate or bivariate with multivariate model estimates for means of *vgll3* genotypes, phenotypic proportion estimates of variance components, and estimates for correlations. Bayesian MCMC univariate (UV) model estimates for maturation probability (**A, F**) and Bayesian MCMC multivariate (MV) model estimates for all five traits (all panels) are shown with posterior-based 95% credible intervals, whereas REML bivariate (BV) model estimates for sex-specific length (**B, C, G, H, I**) or sex-specific condition (**D, E, J, K, L**) are shown with Taylor-series-derived approximate 95% confidence intervals (partly off the plot area for variance proportions or correlations > 1). Variance component proportions are for common environmental variance (c^2; based on tank replicates) or additive genetic variance (h^2; based on expected relatedness among individuals), whereas correlations are for additive genetic correlation (R_G) between temperature environments (**G, H, J, K**) or for common environmental correlation (R_C) and additive genetic correlation (R_G) between sexes within environments (**I, L**). Estimates for the warm environment are in yellow, whereas estimates for the cold environment are in blue. Gray colour indicates between-temperature environment correlations.

Table S1. Dam effects were not detected by likelihood ratio tests (LRT) on the covariance structure in bivariate models for the two traits of male and female length.

Model #	Dam covariance matrix	Description	K	Loglik	AIC	vs. #	ΔAIC	LRT	*P*
0	Dam:Trait:Temperature	unstructured 4x4	32	-335.2	734.4	-	-	-	-
1	Dam:Trait	unstructured 2x2	25	-335.0	719.9	0	14.4	-0.4	1.00
2	Dam:Temperature	unstructured 2x2	25	-335.1	720.1	0	14.2	-0.2	1.00
3	Dam	common variance	23	-335.1	718.0	1	3.6	0.4	0.833
3	Dam	common variance	23	-335.1	718.0	2	3.8	0.2	0.914
4	NA	no dam effects	22	-335.5	2523.7	3	1.3	0.7	0.409

K indicates the total number of covariance parameters in the model
Loglik is the log of the model likelihood
AIC is the Akaike information criterion with a “smaller is better” definition
The model # in bold is the chosen model

Table S2. Dam effects were not detected by likelihood ratio tests (LRT) on the covariance structure in bivariate models for the two traits of male and female condition.

Model #	Dam covariance matrix	Description	K	Loglik	AIC	vs. #	ΔAIC	LRT	*P*
0	Dam:Trait:Temperature	unstructured 4x4	32	-1237.1	2538.3	-	-	-	-
1	Dam:Trait	unstructured 2x2	25	-1238.8	2527.5	0	10.8	3.3	0.861
2	Dam:Temperature	unstructured 2x2	25	-1238.0	2526.0	0	12.3	1.7	0.973
3	Dam	common variance	23	-1238.8	2523.7	1	3.9	0.1	0.936
3	Dam	common variance	23	-1238.8	2523.7	2	3.9	1.7	0.437
4	NA	no dam effects	22	-1239.7	2523.3	3	0.3	1.7	0.196

K indicates the total number of covariance parameters in the model
Loglik is the log of the model likelihood
AIC is the Akaike information criterion with a “smaller is better” definition
The model # in bold is the chosen model